



1/10

## SEQUENCE LISTING

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<110> Tamatani, Takuya  
Tezuka, Katsunari

<120> CELL SURFACE MOLECULE MEDIATING CELL ADHESION AND SIGNAL TRANSMISSION

<130> Q6501/039001

<140> US 09/383,551

<141> 1999-08-26

<150> WO PCT/JP98/00831

<151> 1998-02-21

<150> JP 10/62217

<151> 1998-02-26

<150> JP 9/62290

<151> 1997-02-27

<160> 15

<170> FastSEQ for Windows Version 4.0

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<220>

<221> CDS

<222> (1)...(597)

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1 5 10 15	
ggt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata	96
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile	
20 25 30	
ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc	144
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val	
35 40 45	
cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat	192
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp	
50 55 60	
ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg	240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	
65 70 75 80	
aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta	288
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
85 90 95	

tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca	336
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser	
100 105 110	
att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg	384
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu	
115 120 125	
cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc	432
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro	
130 135 140	
ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt	480
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu	
145 150 155 160	
att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct	528
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro	
165 170 175	
aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct	576
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser	
180 185 190	
aga ctc aca gat gtg acc cta taa	600
Arg Leu Thr Asp Val Thr Leu	
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Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val	
35 40 45	
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp	
50 55 60	
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	
65 70 75 80	
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
85 90 95	
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser	
100 105 110	
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu	
115 120 125	
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro	
130 135 140	
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu	
145 150 155 160	
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro	
165 170 175	
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 tagactcaca gatgtgaccc tataatatgg aactctggca cccaggcatg aagcacgttg 660  
 gccagttttc ctcaacttga agtgcaagat tctcttattt cggggaccac ggagagtctg 720  
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 aaaatcatct ttaatgggac agcattctca tggggtagag cagaatattc atttagcctg 1680  
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Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn	
10 15 20	
gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag	151
Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln	
25 30 35	
att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg	199
Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Leu Lys Met Gln Leu	
40 45 50 55	
ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc	247
Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser	
60 65 70	
gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg	295
Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu	
75 80 85	
tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag	343
Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln	
90 95 100	
ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt	391
Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe	
105 110 115	
caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag	439
Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln	
120 125 130 135	
ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt	487
Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe	
140 145 150	
gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa	535
Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys	
155 160 165	
aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc	583
Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe	
170 175 180	
atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt atg acc	631
Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Met Thr	
185 190 195	
tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttcccct	684
Ser	
200	
gaaacttgaa tggagaaagt cttctatttt ctggaccaca gggcatctga cttgattaac	744
tactgatacc tccttttggk gttttgtttg tctggatcag tgactatcag tcactcggaa	804
tttcagcaga ctgccttggg tttgctgagt ccttttaagg caaaccctt cttatagaag	864
acccgggtca tatgtattca acaaacagac ctactggga tacaatccc tctttctgcg	924
cctgttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttacaaaaa	984

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gacaggttga	aatagycctc	atgascstgg	aacagwactc	cagactgtgc	tggagtccca	1764
aagttaggag	ggccatggag	cctgggacag	gctgctgctt	tggctcttag	gatctaggaa	1824
raattacaga	ggggccaaga	cagagttccc	tcccctagaa	actgtgcagc	ctggaagtca	1884
gccctggcac	tttaagatag	ccttcttttag	aacatgagtt	agttggtagt	attctgacgt	1944
gtaaacagcc	tatkgttgct	cggagctgga	ccattttctc	cacttcctcg	tctgcatgcc	2004
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<220>  
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ctt tta aca gga gaa atc aat ggc tgc gcc gat cat agg atg ttt tca															96	
Leu	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	Ala	Asp	His	Arg	Met	Phe	Ser	
			20					25					30			
ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc															144	
Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val	
		35					40					45				
cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa															192	
Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu	
		50				55					60					
ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca															240	
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro	
		65			70					75				80		
atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta															288	
Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu	
				85					90					95		
aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc															336	
Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser	
			100					105					110			
att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat															384	
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr	
		115					120						125			

ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta 432  
 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
 130 135 140

ccc gta ggg ttg cca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata 480  
 Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
 145 150 155 160

ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac 528  
 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp  
 165 170 175

cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag 576  
 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
 180 185 190

tct aga ctt gca ggt gtg acc tca taa 603  
 Ser Arg Leu Ala Gly Val Thr Ser  
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<210> 6

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<212> DNA

<213> Rattus rattus

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<221> CDS

<222> (35)...(682)

<400> 6

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 Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn  
 10 15 20

gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag 151  
 Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln  
 25 30 35

att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg 199  
 Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu  
 40 45 50 55

ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247  
 Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser  
 60 65 70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295  
 Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu  
 75 80 85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343  
 Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln  
 90 95 100

ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt 391  
 Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe  
 105 110 115

caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag 439  
 Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln  
 120 125 130 135

ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 487  
 Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe  
 140 145 150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535  
 Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys  
 155 160 165

aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc 583  
 Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe  
 170 175 180

atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt aca gca 631  
 Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Thr Ala  
 185 190 195

ccc ctt agg gct ttg ggg aga gga gaa cac tct tca tgt caa gac cgg 679  
 Pro Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg  
 200 205 210 215

aat taatttggtt atttctatatt taaaagaaag acattttttc ccctaaagat 732  
 Asn

aatttttgta tttttatgtg aaagtctgaa ttttcatttt aactcgactt atatactctg 792  
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 <223> synthetically generated primer bind

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<210> 8  
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<210> 13  
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Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val  
35 40 45  
Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp  
50 55 60  
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro  
65 70 75 80  
Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
85 90 95  
Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser  
100 105 110  
Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr  
115 120 125  
Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
130 135 140  
Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile  
145 150 155 160



Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp  
 165 170 175  
 Pro Asn Ser Glu Tyr Met Phe Met Ala Val Asn Thr Asn Lys Lys  
 180 185 190  
 Ser Arg Leu Ala Gly Met Thr Ser  
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 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val  
 35 40 45  
 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
 50 55 60  
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
 65 70 75 80  
 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
 85 90 95  
 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
 100 105 110  
 Ile Phe Asp Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr  
 115 120 125  
 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
 130 135 140  
 Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
 145 150 155 160  
 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp  
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 <213> Rattus rattus

<400> 15  
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 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val  
 35 40 45  
 Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp  
 50 55 60  
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro  
 65 70 75 80  
 Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
 85 90 95  
 Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser  
 100 105 110  
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr  
 115 120 125

10/10

Leu	Leu	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu
130						135					140				
Pro	Val	Gly	Cys	Ala	Ala	Phe	Val	Ala	Ala	Leu	Leu	Phe	Gly	Cys	Ile
145					150					155					160
Phe	Ile	Val	Trp	Phe	Ala	Lys	Lys	Lys	Tyr	Arg	Ser	Ser	Val	His	Asp
				165					170					175	
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys
			180					185					190		
Ser	Arg	Leu	Ala	Gly	Thr	Ala	Pro	Leu	Arg	Ala	Leu	Gly	Arg	Gly	Glu
		195					200					205			
His	Ser	Ser	Cys	Gln	Asp	Arg	Asn								
210						215									

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concl'd